

## **RAW SEQUENCE LISTING**

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Application Serial Number: 10/538, 544  
Source: PCT  
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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/538,544

DATE: 06/21/2005

TIME: 13:45:59

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\06172005\J538544.raw

3 <110> APPLICANT: BASF Aktiengesellschaft  
 7 <120> TITLE OF INVENTION: Malate dehydrogenase as target for herbicides  
 11 <130> FILE REFERENCE: PF 0000 054200  
**C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/538,544**  
**C--> 15 <141> CURRENT FILING DATE: 2005-06-10**  
 15 <160> NUMBER OF SEQ ID NOS: 12  
 19 <170> SOFTWARE: PatentIn version 3.1  
 23 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 673  
 27 <212> TYPE: DNA  
 29 <213> ORGANISM: Nicotiana tabacum  
 33 <400> SEQUENCE: 1

34 gcgccgcta aacctccttg ttctttacg ccagaggaag ctgaatattt aacatcttgt	60
36 atacaatggat gggaaactga agttgtttag gcaaaaactg gtgcgtggtc ggcaactctc	120
38 tctatggcat atgctcggt taaatttgcc gacgcatgtt tgcatggatt gagaggagat	180
40 gctggcattt tagaatgtgc ctttgtgtct tctcaggtga ctgaacttcc attttcgca	240
42 tcaaaaatggat ggcttggccg caacggaggta gaagaaatat acccccattgg tccccctaaat	300
44 gaatacgaga ggtctggct tgagaaggca agggaaagagt tggcaacaag tggcagaag	360
46 ggtgtcaact ttgtaaagaa atgagcagac agctacatga cttccaaaatg atgctttat	420
48 gtgggctata tatctcaaattt ccgcagttcc agaaaataag agtagttct ttcttgatt	480
50 aaaggcataaa tcctgttcta attttctata gattgatgcc ttggcaga aaataaatgt	540
52 actatggat catctaaaat aacaacagtc cccagtgcat gttggacttg caaagtatta	600
54 catccttga agcaaggcgt ttttatggac ttttgacag tatggatatt taaaggcatt	660
56 ggagagcggc cgc	673
59 <210> SEQ ID NO: 2	
61 <211> LENGTH: 1505	
63 <212> TYPE: DNA	
65 <213> ORGANISM: Nicotiana tabacum	
69 <220> FEATURE:	
71 <221> NAME/KEY: CDS	
73 <222> LOCATION: (148)..(1221)	
75 <223> OTHER INFORMATION:	
<b>W--&gt; 79 &lt;400&gt; 2</b>	
80 ctaatacgac tcactatagg gcaaggcgtt gatatcaacgc agagtacgcg gggggggaaac	60
82 aaaattcaat tacttacctt gatttctact acctctcttt ctcataaa ttcaaacaca	120
84 caaattctca agcccaagtc tttagaat atg cag aac ggt gca gag acc tat cga	174
85 Met Gln Asn Gly Ala Glu Thr Tyr Arg	
86 1 5	
88 cga atg gcc acc atc tca gct cac ctt aac ccc tct cct tct tct cat	222
89 Arg Met Ala Thr Ile Ser Ala His Leu Asn Pro Ser Pro Ser Ser His	
90 10 15 20 25	
92 cag atg gag gga ggt gtg ggt ttg agc cga gct aat tgc agg gcg aaa	270
93 Gln Met Glu Gly Val Gly Leu Ser Arg Ala Asn Cys Arg Ala Lys	

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94	30	35	40	
96	ggg ggt tct cca gga ttc aaa gtc gcg atc ttg ggt gct gca gga ggt			318
97	Gly Gly Ser Pro Gly Phe Lys Val Ala Ile Leu Gly Ala Ala Gly Gly			
98	45	50	55	
100	att ggt cag cca ctt gct atg ctt atg aaa acg aat cca ctg gtt tca			366
101	Ile Gly Gln Pro Leu Ala Met Leu Met Lys Thr Asn Pro Leu Val Ser			
102	60	65	70	
104	gtt ctg cat ctt tat gat gtt gcc aat act cct ggt gta act gct gac			414
105	Val Leu His Leu Tyr Asp Val Ala Asn Thr Pro Gly Val Thr Ala Asp			
106	75	80	85	
108	att agc cac atg gac act ggt gcc gtg gta cgt ggt ttt cta ggg cct			462
109	Ile Ser His Met Asp Thr Gly Ala Val Val Arg Gly Phe Leu Gly Pro			
110	90	95	100	105
112	caa caa ttg gaa gat gct ctc act ggc atg gac ctt gta ata atc cct			510
113	Gln Gln Leu Glu Asp Ala Leu Thr Gly Met Asp Leu Val Ile Ile Pro			
114	110	115	120	
116	gct ggt gtt cct aga aaa cca ggc atg aca aga gat gat ctt ttc aac			558
117	Ala Gly Val Pro Arg Lys Pro Gly Met Thr Arg Asp Asp Leu Phe Asn			
118	125	130	135	
120	atc aat gca gga att gtg agg act tta tgt gaa gga att gcc aag tgc			606
121	Ile Asn Ala Gly Ile Val Arg Thr Leu Cys Glu Gly Ile Ala Lys Cys			
122	140	145	150	
124	tgt cct aag gcc att gtt aac ata att agt aat cct gtt aac tct aca			654
125	Cys Pro Lys Ala Ile Val Asn Ile Ile Ser Asn Pro Val Asn Ser Thr			
126	155	160	165	
128	gta cca att gct gca gag gtt ttc aag aag gct ggc acc ttt gat ccg			702
129	Val Pro Ile Ala Ala Glu Val Phe Lys Lys Ala Gly Thr Phe Asp Pro			
130	170	175	180	185
132	agg aga ctg ttg ggc gtg aca atg ctt gat att gtc aga gcc aat aca			750
133	Arg Arg Leu Leu Gly Val Thr Met Leu Asp Ile Val Arg Ala Asn Thr			
134	190	195	200	
136	ttt gtg gct gaa gtt ttg ggg ctt gat cct agg gaa gtg gat gtt cca			798
137	Phe Val Ala Glu Val Leu Gly Leu Asp Pro Arg Glu Val Asp Val Pro			
138	205	210	215	
140	gtt gtg ggg ggt cat gct ggc gtt aca att cta cct ctt ctt tcc cag			846
141	Val Val Gly Gly His Ala Gly Val Thr Ile Leu Pro Leu Ser Gln			
142	220	225	230	
144	gtt aaa cct cct tgt tct ttt acg cca gag gaa act gaa tat tta aca			894
145	Val Lys Pro Pro Cys Ser Phe Thr Pro Glu Glu Thr Glu Tyr Leu Thr			
146	235	240	245	
148	tct cgt ata caa aat ggg gga act gaa gtt gtt gag gca aaa gct ggt			942
149	Ser Arg Ile Gln Asn Gly Gly Thr Glu Val Val Glu Ala Lys Ala Gly			
150	250	255	260	265
152	gct ggt tcg gca act ctc tct atg gca tat gct gcg gtt aaa ttt gcc			990
153	Ala Gly Ser Ala Thr Leu Ser Met Ala Tyr Ala Ala Val Lys Phe Ala			
154	270	275	280	
156	gac gca tgt ttg cat gga ttg aga gga gat gct ggc att gta gaa tgt			1038
157	Asp Ala Cys Leu His Gly Leu Arg Gly Asp Ala Gly Ile Val Glu Cys			
158	285	290	295	

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160	gcc	ttt	gtg	tct	tct	cag	gtg	act	gaa	ctt	cca	ttt	ttc	gca	tca	aaa	1086			
161	Ala	Phe	Val	Ser	Ser	Gln	Val	Thr	Glu	Leu	Pro	Phe	Phe	Ala	Ser	Lys				
162																300	305	310		
164	gta	cgg	ctt	ggc	cgc	aac	gga	gtt	gaa	gaa	ata	tac	ccc	ctt	ggt	ccc	1134			
165	Val	Arg	Leu	Gly	Arg	Asn	Gly	Val	Glu	Glu	Ile	Tyr	Pro	Leu	Gly	Pro				
166																315	320	325		
168	cta	aat	gaa	tac	gag	agg	tct	ggg	ctt	gag	aag	gca	aag	aaa	gag	ctg	1182			
169	Leu	Asn	Glu	Tyr	Glu	Arg	Ser	Gly	Leu	Glu	Lys	Ala	Lys	Lys	Glu	Leu				
170																330	335	340	345	
172	gca	aca	agt	gtt	cag	aag	ggt	gtc	aac	ttt	gta	aag	aaa	tgagcagaca		1231				
173	Ala	Thr	Ser	Val	Gln	Lys	Gly	Val	Asn	Phe	Val	Lys								
174																350	355			
176	gctacatgac	ttccaaaaga	tgcttttatg	tggctatat	atctcaaatc	cgcagttcca											1291			
178	gaaaataaga	gtagttctt	tcttgtatta	aaggcataat	cctgttctaa	ttttctatag											1351			
180	attgatgcct	tggtcagaa	aataaatgtt	ctattggtc	atctaaaata	acaacagtcc											1411			
182	ccagtgcatt	ttggacttgc	aaagtattac	atccttgaa	gcaaggcctt	gttatggact											1471			
184	ttttgacagt	atggatattt	aaaggcattt	gaga													1505			
187	<210>	SEQ ID NO:	3																	
189	<211>	LENGTH:	358																	
191	<212>	TYPE:	PRT																	
193	<213>	ORGANISM:	Nicotiana tabacum																	
197	<400>	SEQUENCE:	3																	
199	Met	Gln	Asn	Gly	Ala	Glu	Thr	Tyr	Arg	Arg	Met	Ala	Thr	Ile	Ser	Ala				
200	1																5	10	15	
203	His	Leu	Asn	Pro	Ser	Pro	Ser	Ser	His	Gln	Met	Glu	Gly	Val	Gly					
204																	20	25	30	
207	Leu	Ser	Arg	Ala	Asn	Cys	Arg	Ala	Lys	Gly	Gly	Ser	Pro	Gly	Phe	Lys				
208																	35	40	45	
211	Val	Ala	Ile	Leu	Gly	Ala	Ala	Gly	Gly	Ile	Gly	Gln	Pro	Leu	Ala	Met				
212																	50	55	60	
215	Leu	Met	Lys	Thr	Asn	Pro	Leu	Val	Ser	Val	Leu	His	Leu	Tyr	Asp	Val				
216																	65	70	75	80
219	Ala	Asn	Thr	Pro	Gly	Val	Thr	Ala	Asp	Ile	Ser	His	Met	Asp	Thr	Gly				
220																	85	90	95	
223	Ala	Val	Val	Arg	Gly	Phe	Leu	Gly	Pro	Gln	Gln	Leu	Glu	Asp	Ala	Leu				
224																	100	105	110	
227	Thr	Gly	Met	Asp	Leu	Val	Ile	Ile	Pro	Ala	Gly	Val	Pro	Arg	Lys	Pro				
228																	115	120	125	
231	Gly	Met	Thr	Arg	Asp	Asp	Leu	Phe	Asn	Ile	Asn	Ala	Gly	Ile	Val	Arg				
232																	130	135	140	
235	Thr	Leu	Cys	Glu	Gly	Ile	Ala	Lys	Cys	Cys	Pro	Lys	Ala	Ile	Val	Asn				
236																	145	150	155	160
239	Ile	Ile	Ser	Asn	Pro	Val	Asn	Ser	Thr	Val	Pro	Ile	Ala	Ala	Glu	Val				
240																	165	170	175	
243	Phe	Lys	Lys	Ala	Gly	Thr	Phe	Asp	Pro	Arg	Arg	Leu	Leu	Gly	Val	Thr				
244																	180	185	190	
247	Met	Leu	Asp	Ile	Val	Arg	Ala	Asn	Thr	Phe	Val	Ala	Glu	Val	Leu	Gly				
248																	195	200	205	
251	Leu	Asp	Pro	Arg	Glu	Val	Asp	Val	Pro	Val	Val	Gly	Gly	His	Ala	Gly				

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252	210	215	220
255	Val Thr Ile Leu Pro Leu Leu Ser Gln Val Lys Pro Pro Cys Ser Phe		
256	225	230	235
259	Thr Pro Glu Glu Thr Glu Tyr Leu Thr Ser Arg Ile Gln Asn Gly Gly		240
260	245	250	255
263	Thr Glu Val Val Glu Ala Lys Ala Gly Ala Gly Ser Ala Thr Leu Ser		
264	260	265	270
267	Met Ala Tyr Ala Ala Val Lys Phe Ala Asp Ala Cys Leu His Gly Leu		
268	275	280	285
271	Arg Gly Asp Ala Gly Ile Val Glu Cys Ala Phe Val Ser Ser Gln Val		
272	290	295	300
275	Thr Glu Leu Pro Phe Phe Ala Ser Lys Val Arg Leu Gly Arg Asn Gly		
276	305	310	315
279	Val Glu Glu Ile Tyr Pro Leu Gly Pro Leu Asn Glu Tyr Glu Arg Ser		320
280	325	330	335
283	Gly Leu Glu Lys Ala Lys Lys Glu Leu Ala Thr Ser Val Gln Lys Gly		
284	340	345	350
287	Val Asn Phe Val Lys Lys		
288	355		
291	<210> SEQ ID NO: 4		
293	<211> LENGTH: 16		
295	<212> TYPE: DNA		
297	<213> ORGANISM: Artificial Sequence		
301	<220> FEATURE:		
303	<223> OTHER INFORMATION: Primer		
305	<400> SEQUENCE: 4		
306	agaattcgcg gccgct		16
309	<210> SEQ ID NO: 5		
311	<211> LENGTH: 32		
313	<212> TYPE: DNA		
315	<213> ORGANISM: Artificial Sequence		
319	<220> FEATURE:		
321	<223> OTHER INFORMATION: Primer		
323	<400> SEQUENCE: 5		
324	ctcatgcggc cgcgcaac gcaattaatg tg		32
327	<210> SEQ ID NO: 6		
329	<211> LENGTH: 32		
331	<212> TYPE: DNA		
333	<213> ORGANISM: Artificial Sequence		
337	<220> FEATURE:		
339	<223> OTHER INFORMATION: Primer		
341	<400> SEQUENCE: 6		
342	tcatgcggcc gcgagatcca gttcgatgtac		32
345	<210> SEQ ID NO: 7		
347	<211> LENGTH: 21		
349	<212> TYPE: DNA		
351	<213> ORGANISM: Artificial Sequence		
355	<220> FEATURE:		
357	<223> OTHER INFORMATION: Primer		

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359 <400> SEQUENCE: 7  
360 gtggattgat gtatatctc c 21  
363 <210> SEQ ID NO: 8  
365 <211> LENGTH: 21  
367 <212> TYPE: DNA  
369 <213> ORGANISM: Artificial Sequence  
373 <220> FEATURE:  
375 <223> OTHER INFORMATION: Primer  
377 <400> SEQUENCE: 8  
378 gtaaggatct gagctacaca t 21  
381 <210> SEQ ID NO: 9  
383 <211> LENGTH: 17  
385 <212> TYPE: DNA  
387 <213> ORGANISM: Artificial Sequence  
391 <220> FEATURE:  
393 <223> OTHER INFORMATION: Primer  
395 <400> SEQUENCE: 9  
396 atgagggcgaa aagggggg 17  
399 <210> SEQ ID NO: 10  
401 <211> LENGTH: 25  
403 <212> TYPE: DNA  
405 <213> ORGANISM: Artificial Sequence  
409 <220> FEATURE:  
411 <223> OTHER INFORMATION: Primer  
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414 ttctttaca aagttgacac ctttc 25  
417 <210> SEQ ID NO: 11  
419 <211> LENGTH: 17  
421 <212> TYPE: DNA  
423 <213> ORGANISM: Artificial Sequence  
427 <220> FEATURE:  
429 <223> OTHER INFORMATION: Primer  
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435 <210> SEQ ID NO: 12  
437 <211> LENGTH: 21  
439 <212> TYPE: DNA  
441 <213> ORGANISM: Artificial Sequence  
445 <220> FEATURE:  
447 <223> OTHER INFORMATION: Primer  
449 <400> SEQUENCE: 12  
450 ttcttcgca aaggtaaacac c 21

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/538,544

DATE: 06/21/2005

TIME: 13:46:00

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\06172005\J538544.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:79 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:75